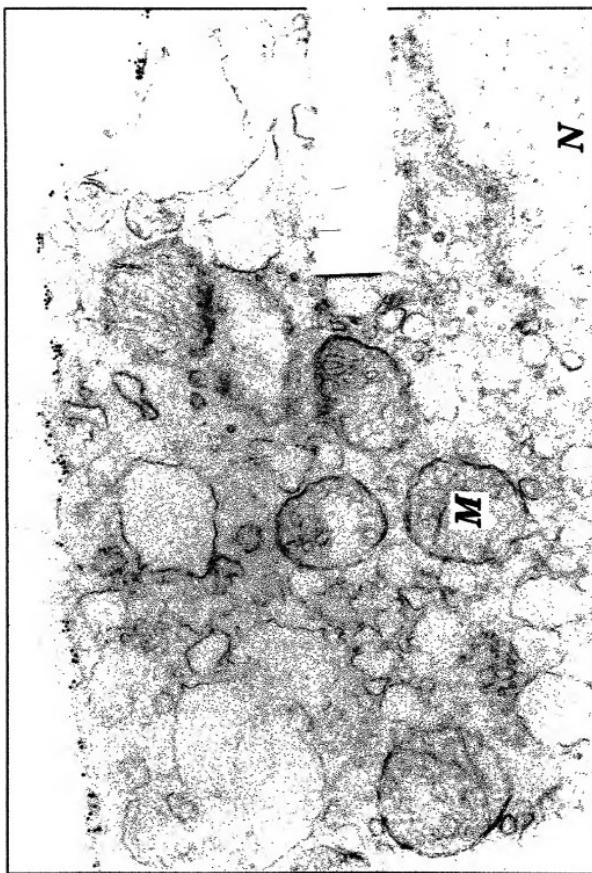
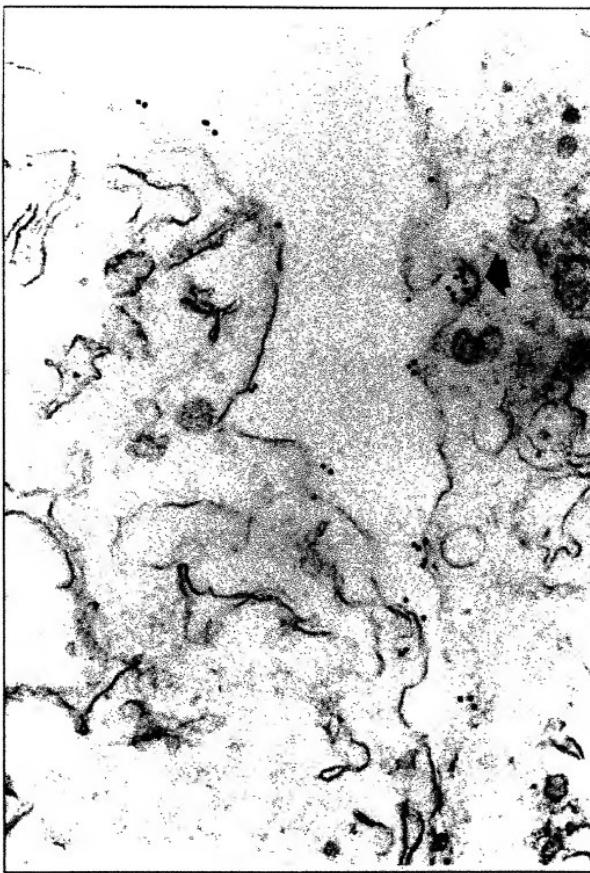


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**FIG. 1**

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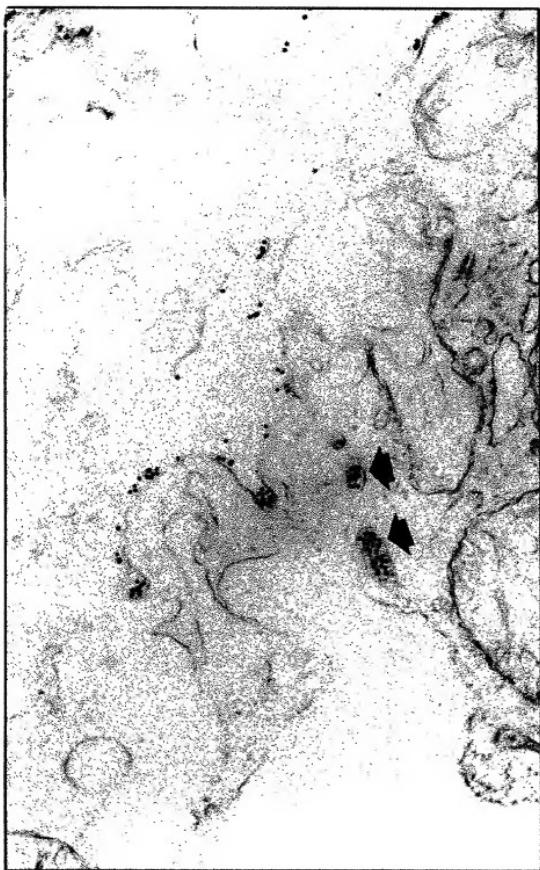
**FIG. 2**

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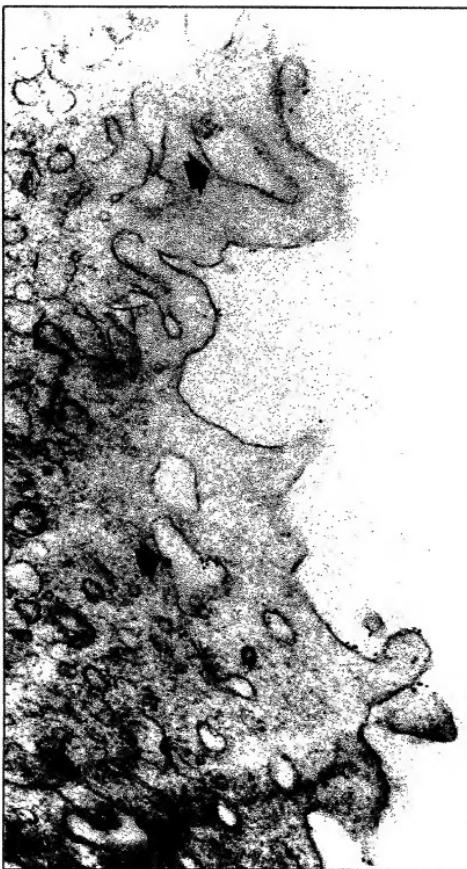
**FIG. 3**

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**FIG. 4**

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**FIG. 5**

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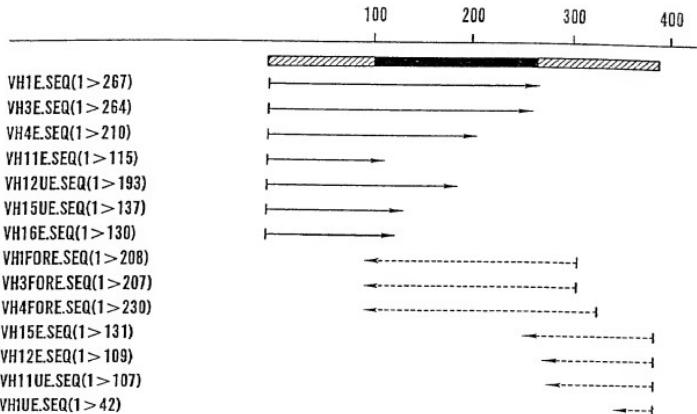


FIG. 6

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ENZYMES: ALL 74 ENZYMES (NO FILTER)

SETTINGS: LINEAR. CERTAIN SITES ONLY. STANDARD GENETIC CODE

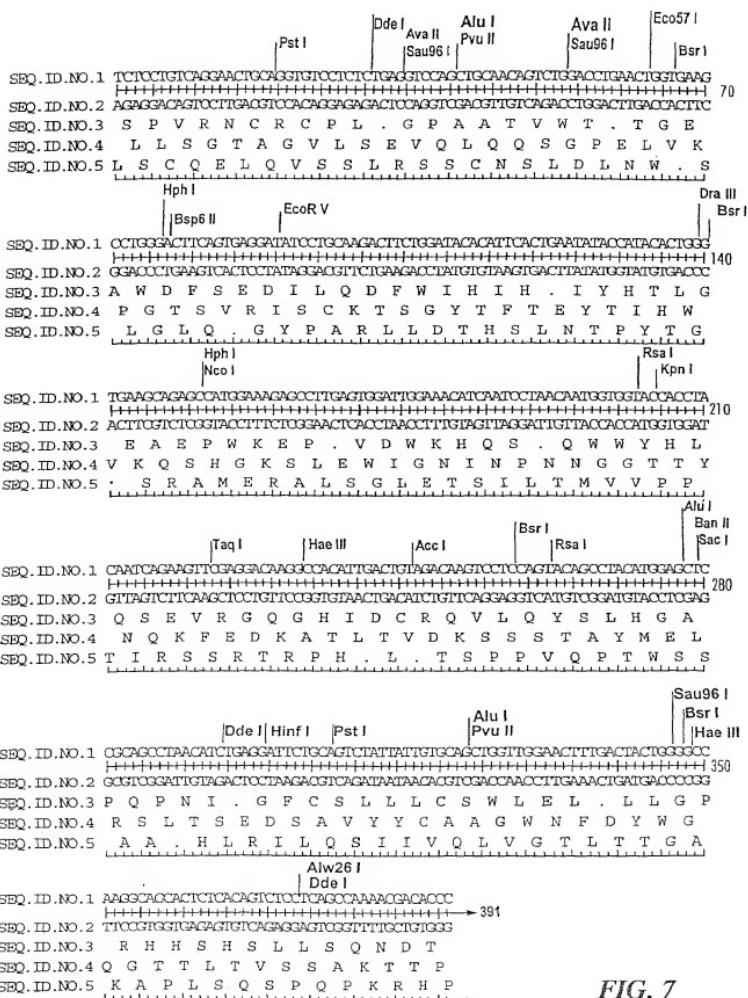


FIG. 7

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LIPMAN-PEARSON PROTEIN ALIGNMENT  
 KTUPLE: 2; GAP PENALTY: 4; GAP LENGTH PENALTY: 12

SEQ1(1>115) J591VH.PRO	SEQ2(1>125) MUVHIIA.PRO	SIMILARITY INDEX	GAP NUMBER	GAP LENGTH	CONSENSUS LENGTH
(1>115)	(1>125)	75.6	2	10	125

EVQLQQSGPELVKPGIVSVRISCKTSGYIFTIETYII-HWVKQSHGKSLEWIGNINPANGGIT  
 EVQLQQSGPELVKPG:SV:ISCK:SGYIFT:Y : :WVKQS.GKSLEWIG:INP.NGGT:  
 EVQLQQSGPELVKPGASVCLISCKASGYIFTIDYYMMNNWVKQSGGKSLEWIGDINPANGGIS

YNQKPFEDKAILIVDKSSSTAYMLRSLSITSEDSEAVYYCAAG-----WNFDYWGGIT  
 YNQKP: :KAIILIVDKSSSTAYML.SLITSEDSEAVYYCA G ..FDYWGGIT  
 YNQKPFGKAILIVDKSSSTAYMLRSLSITSEDSEAVYYCARGYSSSMAYARDYWGGIT

LIVSS  
 :TVSS  
 VIVSS

FIG. 8

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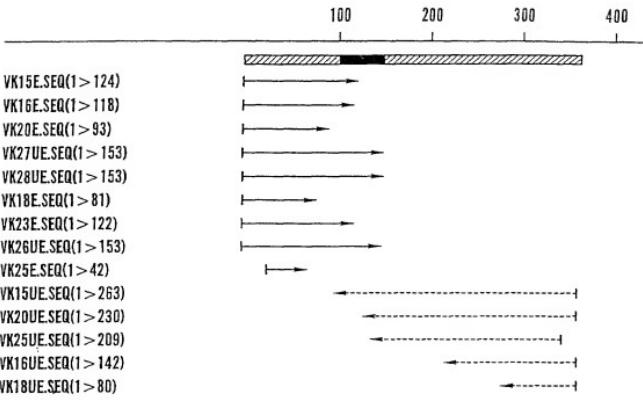


FIG. 9

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ENZYME: ALL 74 ENZYMES (NO FILTER):  
 SETTINGS: LINEAR, CERTAIN SITES ONLY, STANDARD GENETIC CODE

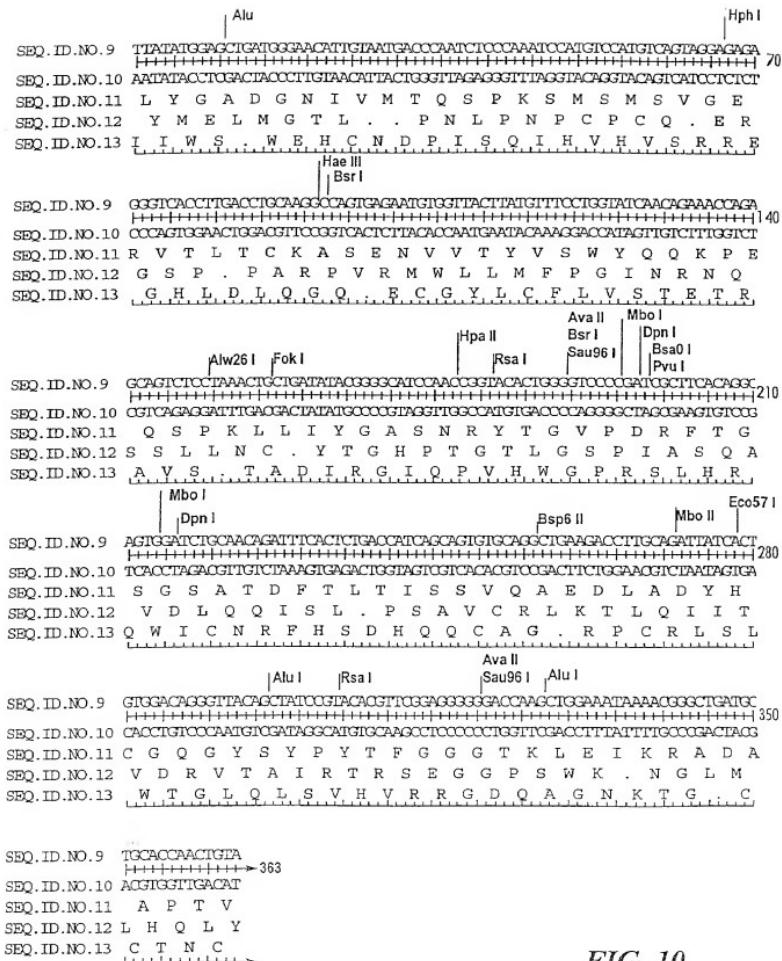


FIG. 10

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LIPMAN-PEARSON PROTEIN ALIGNMENT  
KTUPLE: 2; GAP PENALTY: 4; GAP LENGTH PENALTY: 12

SEQ1(1>107) J591VK.PRO	SEQ2(1>111) MUVK.V.PRO	SIMILARITY INDEX	GAP NUMBER	GAP LENGTH	CONSENSUS LENGTH
(1>107)	(1>109)	60.4	2	2	109

NIVMTQSPKMSMSVGERVTITCKAS-ENVVITYVSWYQQKPQSPKLLIYGASNRYTGVP  
: I M T Q S P . S : S S : G : R V T : T C : A S : : : . Y : W Y Q Q K P . S P K L L I Y A S . . : G V P  
DIQMTOQSPSSLSASLGDRVITTCRASQDDISNYLNWYQQKPGGSPKLLIYYASRLHSGVP

↑ 10              ↓ 20              ↓ 30              ↓ 40              ↓ 50  
↑ 10              ↓ 20              ↑ 30              ↑ 40              ↓ 50              ↓ 60

DRFTGGGSATIDPTLTISSVQAEQLADYHCGGGSY-PYTFCGGTKEIK  
.RF:GSGS:TD:;LTIS:;;ED:A.Y C QG : P T F G G T K L E I K  
SRFSGGGSGGIDYSLTISNLIEDIAITYFCQCGNITLPRTFGGGTKEIK

↑ 60              ↓ 70              ↓ 80              ↓ 90              ↓ 100  
↑ 70              ↑ 80              ↑ 90              ↑ 100

FIG. 11

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